

WEST Search History

DATE: Tuesday, June 22, 2004

Hide?	Set Name	Query	Hit Count
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; THES=ASSIGNEE; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L8	L6 same (substitution\$)	15
<input type="checkbox"/>	L7	L6 same (i adj domain)	24
<input type="checkbox"/>	L6	L5 same integrin	714
<input type="checkbox"/>	L5	baised or open or closed or conformation	4222229
<input type="checkbox"/>	L4	SPRINGER-TIMOTHY.in.	7
<input type="checkbox"/>	L3	SHIMAOKA-MOTOMU.in.	2
<input type="checkbox"/>	L2	SHIFMAN-JULIA.in.	1
<input type="checkbox"/>	L1	MAYO-STEPHEN.in.	8

END OF SEARCH HISTORY

=> d his

(FILE 'HOME' ENTERED AT 13:01:33 ON 22 JUN 2004)

FILE 'DISSABS, IMOBILITY, AGRICOLA, AQUASCI, BIOTECHNO, COMPENDEX,
COMPUAB, CONF, CONFSCI, ELCOM, HEALSAFE, IMSDRUGCONF, LIFESCI, OCEAN,
MEDICONF, PASCAL, PAPERCHEM2, POLLUAB, SOLIDSTATE, ADISCTI, ADISINSIGHT,
ADISNEWS, ANABSTR, BIOBUSINESS, BIOCOMMERCE, ...' ENTERED AT 13:01:50 ON
22 JUN 2004

L1 E MAYO STEPHEN?/AU
 3 S E1 OR E2
 E SHIFMAN JULIA?/AU
L2 16 S E1 OR E2
 E SHIMAOKA MOTOMU?/AU
L3 153737 S E 2
L4 96 S E2
 E SPRINGER TIMOTHY?/AU
L5 4367 S (OPEN OR CLOSED OR CONFORMATION) (S) INTEGRIN?
L6 308 S L5 (S) (I (A) DOMAIN)
L7 104 DUP REM L6 (204 DUPLICATES REMOVED)
L8 19 S L7 AND (139 OR 153 OR 157 OR 160 OR 215)

=>

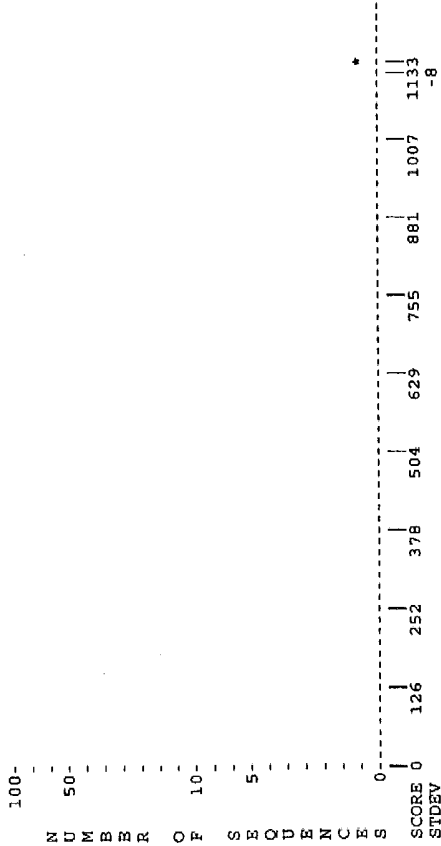
> O <
O | JO IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-902-481b-1.res made by jdelaval on Tue 22 Jun 104 7:02:54-PDT.

Query sequence being compared: US-09-902-481B-1 (1-1153)
Number of sequences searched: 4
Number of scores above cutoff: 4

Results of the initial comparison of US-09-902-481B-1 (1-1153) with:
File : seq3-seq4-seq5-seq6.pap



PARAMETERS

Similarity matrix Unitary K-tuple 2
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 32
Gap size penalty 0.05
Cutoff score 0
Randomization group 0

SEARCH STATISTICS

Scores: Mean 1128 Median 1129 Standard Deviation 3.70
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00
Number of residues: 4548
Number of sequences searched: 4
Number of scores above cutoff: 4

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Sig.	Frame
1. US-09-902-481B-6	Sequence 6, Application U 1137 1133	1133	1.35	0	
2. US-09-902-481B-5	Sequence 5, Application U 1137 1129	1129	0.27	0	
3. US-09-902-481B-4	Sequence 4, Application U 1137 1128	1128	0.00	0	
4. US-09-902-481B-3	Sequence 3, Application U 1137 1124	1124	-1.08	0	

1. US-09-902-481B-1 (1-1153)
US-09-902-481B-6 Sequence 6, Application US/09902481B

Sequence 6, Application US/09902481B

GENERAL INFORMATION:

APPLICANT: Springer, Timothy

APPLICANT: Shimaoka, Motomu

APPLICANT: Shifman, Julia

APPLICANT: Mayo, Stephen

TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY

FILE REFERENCE: A-70586-1/RPT/RMS/RMK

CURRENT APPLICATION NUMBER: US/09/902,481B

CURRENT FILING DATE: 2001-07-09

PRIOR APPLICATION NUMBER: US 60/216,600

PRIOR FILING DATE: 2000-07-07

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6

LENGTH: 1137

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: synthetic

Initial Score = 1133 Optimized Score = 1133 Significance = 1.35
Residue Identity = 99% Matches = 1133 Mismatches = 4
Gaps = 0 Conservative Substitutions = 0

10 X 20 30 40 50 60 70
MALRVLLTALTCHEGPNLDTENAMTFQENARGFGQSVVLOGSRVVGAPQEIIVAAVORGSLYQCDYSTGS
X
80 90 100 110 120 130 140
CEPIRLQVPEAVNMSLGLSLAATTSPPOLLACGPTVHOTCSENTVVKGLCPFLGSLNLRQQPKPFALRGC
60 70 80 90 100 110 120
CEPIRLQVPEAVNMSLGLSLAATTSPPOLLACGPTVHOTCSENTVVKGLCPFLGSLNLRQQPKPFALRGC
150 160 170 180 190 200 210
PQSDIAFLIDGSGSIIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTPFKEFQNNPRLSVK
130 140 150 160 170 180 190 200
PQSDIAFLIDGSGSIIIPHDPRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTPFKEFQNNPRLSVK
220 230 240 250 260 270 280
PITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFDPLGYEDVTPEDRBSGVIYVIGVG
210 220 230 240 250 260 270
PITQLGRTHATGIRKVVRELFNITNGARKNAFKILVITDGEKFDPLGYEDVTPEDRBSGVIYVIGVG
290 300 310 320 330 340 350 360
DAFRSEKSRQELNTIAKPPRDHVQVQNNPFAKLTIONQLREKIIFAIEGTQTSSSPHEHMQEFSAAIT
280 290 300 310 320 330 340
DAFRSEKSRQELNTIAKPPRDHVQVQNNPFAKLTIONQLREKIIFAIEGTQTSSSPHEHMQEFSAAIT
370 380 390 400 410 420 430
SNGPLLSTVGSYDWAGVFLYTSKEKSTPINTVRVSDNDAYLGLAAAILLRNVOSLVLGAPRYCHIGLV

Sequence 5, Application US/09902481B
GENERAL INFORMATION:
APPLICANT: Springer, Timothy
APPLICANT: Shimada, Motomu
APPLICANT: Shifman, Julia
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/902,481B
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/216,600
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 1137
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
Initial Score = 1129 Optimized Score = 1129 Significance = 0.27
Residue Identity = 93% Matches = 1129 Mismatches = 8
Gaps = 0 Conservative Substitutions = 0
X 20 30 40 50 60 70
MALRVLLTALTLCHEFNLTENAMTQENARGFQSVVQLQSSRVVVGAPQEIIVAAANQSGSLYCQDYSTGS
|||||
FNLTENAMTQENARGFQSVVQLQSSRVVVGAPQEIIVAAANQSGSLYCQDYSTGS
X 10 20 30 40 50
CEPIRLQVPVEAVNMVSLGLSLAATSPQALLACGPTVHTCSENTYVYKGLCFPLGSLNRQOPQFPPEALRGC
|||||
CEPIRLQVPVEAVNMVSLGLSLAATSPQALLACGPTVHTCSENTYVYKGLCFPLGSLNRQOPQFPPEALRGC
60 70 80 90 100 110 120 130 140
POEDSDIAFLDGGSGSIIPHDPRMKEFVSTVMEQLKSKTLPFLMQLVSEEFRIHTFKFQNNPNRSLVK
|||||
POEDSDIAFLDGGSGSIIPHDPRMKEFVSTVMEQLKSKTLPFLMQLVSEEFRIHTFKFQNNPNRSLVK
130 140 150 160 170 180 190 200
PITQLLGHRTATGIRKVVRELFNITNGARKNAFKILITDGEKFGDPLGYEDVIPADREGVIRYVIGVG
|||||
PITQLLGHRTATGIRKVVRELFNITNGARKNAFKILITDGEKFGDPLGYEDVIPADREGVIRYVIGVG
210 220 230 240 250 260 270
DAFSEKSRQELNTIASKPPRDHVPQNNPEALKTIONLREKIPATEGTOTGSSSSPEHEMSQBFSAAIT
|||||
DAFSEKSRQELNTIASKPPRDHVPQNNPEALKTIONLREKIPATEGTOTGSSSSPEHEMSQBFSAAIT
280 290 300 310 320 330 340
SNGPLLSVGSVDWAGGVFLYTSKEKSTFINMTVDSDMDNDAYILGYAAAILLRNVQSLVGLGAPRYQHIGLV
|||||
SNGPLLSVGSVDWAGGVFLYTSKEKSTFINMTVDSDMDNDAYILGYAAAILLRNVQSLVGLGAPRYQHIGLV
350 360 370 380 390 400 410 420 430
AMFRONTGWESNANVKGTQIGAYFGASLCSVDVDSNGSDTLVILGAPHYYEQTGCGVSVCPPLRGRARW
|||||
AMFRONTGWESNANVKGTQIGAYFGASLCSVDVDSNGSDTLVILGAPHYYEQTGCGVSVCPPLRGRARW
440 450 460 470 480 490 500
QCDVLYGEGQGPWCFRFGAALTVLGDVNGDKLTDAIICAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSK
|||||
QCDVLYGEGQGPWCFRFGAALTVLGDVNGDKLTDAIICAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSK
510 520 530 540 550 560 570
QCDVLYGEGQGPWCFRFGAALTVLGDVNGDKLTDAIICAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSK
|||||
QCDVLYGEGQGPWCFRFGAALTVLGDVNGDKLTDAIICAPGEEDNRGAVYLFHGTSGSGISPSHSQRIAGSK
580 590 600 610 620 630 640
LSPLRQYFQGSLSGGQDLTMDGLVLTGACQGHVLLRSQPVLRVKAIMEFNPREVARNFECNDQVVKGE
|||||
LSPLRQYFQGSLSGGQDLTMDGLVLTGACQGHVLLRSQPVLRVKAIMEFNPREVARNFECNDQVVKGE
650 660 670 680 690 700 710 720 730 740 750 760 770 780 790
AGEVRVCLHVQKSTDRRLREGQIQSVTVYDLALDSGRPHSRAVFNETKNSTRQTQVILGLTQTCETLKLQLP
|||||
AGEVRVCLHVQKSTDRRLREGQIQSVTVYDLALDSGRPHSRAVFNETKNSTRQTQVILGLTQTCETLKLQLP
800 810 820 830 840 850 860 870 880 890 900 910 920 930
LVVGGPREFNVTTVVRNDGEDSYRTQVTPFFPLDLSYRKVSTLQNRQSRWRLACESASSTEVSGALKSTIS
|||||
LVVGGPREFNVTTVVRNDGEDSYRTQVTPFFPLDLSYRKVSTLQNRQSRWRLACESASSTEVSGALKSTIS
940 950 960 970 980 990 1000
TKYLNTASNTSRVMOHQYQSNLCORSIPISLAVFLVPLNQTVIDRPOVTFSENLSSTCHTKERLPSH
|||||
TKYLNTASNTSRVMOHQYQSNLCORSIPISLAVFLVPLNQTVIDRPOVTFSENLSSTCHTKERLPSH
1010 1020 1030 1040 1050 1060 1070 1080
SDFLAELRAPVNCISIAVCORIQCDIPFGIQEENATLKNLSFDWIKTSHNHLITVSTAEILFNDVSF
|||||
SDFLAELRAPVNCISIAVCORIQCDIPFGIQEENATLKNLSFDWIKTSHNHLITVSTAEILFNDVSF
1090 1100 1110 1120 1130 1140 1150
TLLPGQAFVRSOTETKVPFEPVNPPLIVGSSVGGILLALITAAIKLGFPPKQYQDMMSSEGPPCAEP
|||||
TLLPGQAFVRSOTETKVPFEPVNPPLIVGSSVGGILLALITAAIKLGFPPKQYQDMMSSEGPPCAEP
1070 1080 1090 1100 1110 1120 1130
TLLPGQAFVRSOTETKVPFEPVNPPLIVGSSVGGILLALITAAIKLGFPPKQYQDMMSSEGPPCAEP
|||||
TLLPGQAFVRSOTETKVPFEPVNPPLIVGSSVGGILLALITAAIKLGFPPKQYQDMMSSEGPPCAEP
1160 1170 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800 1810 1820 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920 1930 1940 1950 1960 1970 1980 1990 2000 2010 2020 2030 2040 2050 2060 2070 2080 2090 2100 2110 2120 2130 2140 2150 2160 2170 2180 2190 2200 2210 2220 2230 2240 2250 2260 2270 2280 2290 2300 2310 2320 2330 2340 2350 2360 2370 2380 2390 2400 2410 2420 2430 2440 2450 2460 2470 2480 2490 2500 2510 2520 2530 2540 2550 2560 2570 2580 2590 2600 2610 2620 2630 2640 2650 2660 2670 2680 2690 2700 2710 2720 2730 2740 2750 2760 2770 2780 2790 2800 2810 2820 2830 2840 2850 2860 2870 2880 2890 2900 2910 2920 2930 2940 2950 2960 2970 2980 2990 3000 3010 3020 3030 3040 3050 3060 3070 3080 3090 3100 3110 3120 3130 3140 3150 3160 3170 3180 3190 3200 3210 3220 3230 3240 3250 3260 3270 3280 3290 3300 3310 3320 3330 3340 3350 3360 3370 3380 3390 3400 3410 3420 3430 3440 3450 3460 3470 3480 3490 3500 3510 3520 3530 3540 3550 3560 3570 3580 3590 3600 3610 3620 3630 3640 3650 3660 3670 3680 3690 3700 3710 3720 3730 3740 3750 3760 3770 3780 3790 3800 3810 3820 3830 3840 3850 3860 3870 3880 3890 3900 3910 3920 3930 3940 3950 3960 3970 3980 3990 4000 4010 4020 4030 4040 4050 4060 4070 4080 4090 4100 4110 4120 4130 4140 4150 4160 4170 4180 4190 4200 4210 4220 4230 4240 4250 4260 4270 4280 4290 4300 4310 4320 4330 4340 4350 4360 4370 4380 4390 4400 4410 4420 4430 4440 4450 4460 4470 4480 4490 4500 4510 4520 4530 4540 4550 4560 4570 4580 4590 4600 4610 4620 4630 4640 4650 4660 4670 4680 4690 4700 4710 4720 4730 4740 4750 4760 4770 4780 4790 4800 4810 4820 4830 4840 4850 4860 4870 4880 4890 4900 4910 4920 4930 4940 4950 4960 4970 4980 4990 5000 5010 5020 5030 5040 5050 5060 5070 5080 5090 5100 5110 5120 5130 5140 5150 5160 5170 5180 5190 5200 5210 5220 5230 5240 5250 5260 5270 5280 5290 5300 5310 5320 5330 5340 5350 5360 5370 5380 5390 5400 5410 5420 5430 5440 5450 5460 5470 5480 5490 5500 5510 5520 5530 5540 5550 5560 5570 5580 5590 5600 5610 5620 5630 5640 5650 5660 5670 5680 5690 5700 5710 5720 5730 5740 5750 5760 5770 5780 5790 5800 5810 5820 5830 5840 5850 5860 5870 5880 5890 5900 5910 5920 5930 5940 5950 5960 5970 5980 5990 6000 6010 6020 6030 6040 6050 6060 6070 6080 6090 6100 6110 6120 6130 6140 6150 6160 6170 6180 6190 6200 6210 6220 6230 6240 6250 6260 6270 6280 6290 6300 6310 6320 6330 6340 6350 6360 6370 6380 6390 6400 6410 6420 6430 6440 6450 6460 6470 6480 6490 6500 6510 6520 6530 6540 6550 6560 6570 6580 6590 6600 6610 6620 6630 6640 6650 6660 6670 6680 6690 6700 6710 6720 6730 6740 6750 6760 6770 6780 6790 6800 6810 6820 6830 6840 6850 6860 6870 6880 6890 6900 6910 6920 6930 6940 6950 6960 6970 6980 6990 7000 7010 7020 7030 7040 7050 7060 7070 7080 7090 7100 7110 7120 7130 7140 7150 7160 7170 7180 7190 7200 7210 7220 7230 7240 7250 7260 7270 7280 7290 7300 7310 7320 7330 7340 7350 7360 7370 7380 7390 7400 7410 7420 7430 7440 7450 7460 7470 7480 7490 7500 7510 7520 7530 7540 7550 7560 7570 7580 7590 7600 7610 7620 7630 7640 7650 7660 7670 7680 7690 7700 7710 7720 7730 7740 7750 7760 7770 7780 7790 7800 7810 7820 7830 7840 7850 7860 7870 7880 7890 7900 7910 7920 7930 7940 7950 7960 7970 7980 7990 8000 8010 8020 8030 8040 8050 8060 8070 8080 8090 8100 8110 8120 8130 8140 8150 8160 8170 8180 8190 8200 8210 8220 8230 8240 8250 8260 8270 8280 8290 8300 8310 8320 8330 8340 8350 8360 8370 8380 8390 8400 8410 8420 8430 8440 8450 8460 8470 8480 8490 8500 8510 8520 8530 8540 8550 8560 8570 8580 8590 8600 8610 8620 8630 8640 8650 8660 8670 8680 8690 8700 8710 8720 8730 8740 8750 8760 8770 8780 8790 8800 8810 8820 8830 8840 8850 8860 8870 8880 8890 8900 8910 8920 8930 8940 8950 8960 8970 8980 8990 9000 9010 9020 9030 9040 9050 9060 9070 9080 9090 9100 9110 9120 9130 9140 9150 9160 9170 9180 9190 9200 9210 9220 9230 9240 9250 9260 9270 9280 9290 9300 9310 9320 9330 9340 9350 9360 9370 9380 9390 9400 9410 9420 9430 9440 9450 9460 9470 9480 9490 9500 9510 9520 9530 9540 9550 9560 9570 9580 9590 9600 9610 9620 9630 9640 9650 9660 9670 9680 9690 9700 9710 9720 9730 9740 9750 9760 9770 9780 9790 9800 9810 9820 9830 9840 9850 9860 9870 9880 9890 9900 9910 9920 9930 9940 9950 9960 9970 9980 9990 10000 10010 10020 10030 10040 10050 10060 10070 10080 10090 10100 10110 10120 10130 10140 10150 10160 10170 10180 10190 10200 10210 10220 10230 10240 10250 10260 10270 10280 10290 10300 10310 10320 10330 10340 10350 10360 10370 10380 10390 10400 10410 10420 10430 10440 10450 10460 10470 10480 10490 10500 10510 10520 10530 10540 10550 10560 10570 10580 10590 10600 10610 10620 10630 10640 10650 10660 10670 10680 10690 10700 10710 10720 10730 10740 10750 10760 10770 10780 10790 10800 10810 10820 10830 10840 10850 10860 10870 10880 10890 10900 10910 10920 10930 10940 10950 10960 10970 10980 10990 11000 11010 11020 11030 11040 11050 11060 11070 11080 11090 11100 11110 11120 11130 11140 11150 11160 11170 11180 11190 11200 11210 11220 11230 11240 11250 11260 11270 11280 11290 11300 11310 11320 11330 11340 11350 11360 11370 11380 11390 11400 11410 11420 11430 11440 11450 11460 11470 11480 11490 11500 11510 11520 11530 11540 11550 11560 11570 11580 11590 11600 11610 11620 11630 11640 11650 11660 11670 11680 11690 11700 11710 11720 11730 11740 11750 11760 11770 11780 11790 11800 11810 11820 11830 11840 11850 11860 11870 11880 11890 11900 11910 11920 11930 11940 11950 11960 11970 11980 11990 12000 12010 12020 12030 12040 12050 12060 12070 12080 12090 12100 12110 12120 12130 12140 12150 12160 12170 12180 12190 12200 12210 12220 12230 12240 12250 12260 12270 12280 12290 12300 12310 12320 12330 12340 12350 12360 12370 12380 12390 12400 12410 12420 12430 12440 12450 12460 12470 12480 12490 12500 12510 12520 12530 12540 12550 12560 12570 12580 12590 12600 12610 12620 12630 12640 12650 12660 12670 12680 12690 12700 12710 12720 12730 12740 12750 12760 12770 12780 12790 12800 12810 12820 12830 12840 12850 12860 12870 12880 12890 12900 12910 12920 12930 12940 12950 12960 12970 12980 12990 13000 13010 13020 13030 13040 13050 13060 13070 13080 13090 13100 13110 13120 13130 13140 13150 13160 13170 13180 13190 13200 13210 13220 13230 13240 13250 13260 13270 13280 13290 13300 13310 13320 13330 13340 13350 13360 13370 13380 13390 13400 13410 13420 13430 13440 13450 13460 13470 13480 13490 13500 13510 13520 13530 13540 13550 13560 13570 13580 13590 13600 13610 13620 13630 13640 13650 13660 13670 13680 13690 13700 13710 13720 13730 13740 13750 13760 13770 13780 13790 13800 13810 13820 13830 13840 13850 13860 13870 13880 13890 13900 13910 13920 13930 13940 13950 13960 13970 13980 13990 14000 14010 14020 14030 14040 14050 14060 14070 14080 14090 14100 14110 14120 14130 14140 14150 14160 14170 14180 14190 14200 14210 14220 14230 14240 14250 14260 14270 14280 14290 14300 14310 14320 14330 14340 14350 14360 14370 14380 14390 14400 14410 14420 14430 14440 14450 14460 14470 14480 14490 14500 14510 14520 14530 14540 14550 14560 14570 14580 14590 14600 14610 14620 14630 14640 14650 14660 14670 14680 14690 14700 14710 14720 14730 14740 14750 14760 14770 14780 14790 14800 14810 14820 14830 14840 14850 14860 14870 14880 14890 14900 14910 14920 14930 14940 14950 14960 14970 14980 14990 15000 15010 15020 15030 15040 15050 15060 15070 15080 15090 15100 15110 15120 15130 15140 15150 15160 15170 15180 15190 15200 15210 15220 15230 15240 15250 15260 15270 15280 15290 15300 15310 15320 15330 15340 15350 15360 15370 15380 15390 15400 15410 15420 15430 15440 15450 15460 15470 15480 15490 15500 15510 15520 15530 15540 15550 15560 15570 15580 15590 15600 15610 15620 15630 15640 15650 15660 15670 15680 15690 15700 15710 15720 15730 15740 15750 15760 15770 15780 15790 15800 15810 15820 15830 15840 15850 15860 15870 15880 15890 15900 15910 15920 15930 15940 15950 15960 15970 15980 15990 16000 16010 16020 16030 16040 16050 16060 16070 16080 16090 16100 16110 16120 16130 16140 16150 16160 16170 16180 16190 16200 16210 16220 16230 16240 16250 16260 16270 16280 16290 16300 16310 16320 16330 16340 16350 16360 16370 16380 16390 16400 16410 16420 16430 16440 16450 16460 16470 16480 16490 16500 16510 16520 16530 16540 16550 16560 16570 16580 16590 16600 16610 16620 16630 16640 16650 16660 16670 16680 16690 16700 16710 16720 16730 16740 16750 16760 16770 16780 16790 16800 16810 16820 16830 16840 16850 16860 16870 16880 16890 16900 16910 16920 16930 16940 16950 16960 16970 16980 16990 17000 17010 17020 17030 17040 17050 17060 17070 17080 17090 17100 17110 17120 17130 17140 17150 17160 17170 17180 17190 17200 17210 17220 17230 17240 17250 17260 17270 17280 17290 17300 17310 17320 17330 17340 17350 17360 17370 17380 17390 17400 17410 17420 17430 17440 17450 17460 17470 17480 17490 17500 17510 17520 17530 17540 17550 17560 17570 17580 17590 17600 17610 17620 17630 17640 17650 17660 17670 17680 17690 17700 17710 17720 17730 17740 17750 17760 17770 17780 17790 17800 17810 17820 17830 17840 17850 17860 17870 17880 17890 17900 17910 17920 17930 17940 17950 17960 17970 17980 17990 18000 18010 18020 18030 18040 18050 18060 18070 18080 18090 18100 18110 18120 18130 18140 18150 18160 18170 18180 18190 18200 18210 18220 18230 18240 18250 18260 18270 18280 18290 18300 18310 18320 18330 18340 18350 18360 18370 18380 18390 18400 18410 18420 18430 18440 18450 18460 18470 18480 18490 18500 18510 18520 18530 18540 18550 18560 18570 18580 18590 18600 18610 18620 18630 18640 18650 18660 18670 18680 18690 18700 18710 18720 18730 18740 18750 18760 18770 18780 18790 18800 18810 18820 18830 18840 18850 18860 18870 18880 18890 18900 18910 18920 18930 18940 18950 18960 18970 18980 18990 19000 19010 19020 19030 19040 19050 19060 19070 19080 19090 19100 19110 19120 19130 19140 19150 19160 19170 19180 19190 19200 19210 19220 19230 1

580 590 600 610 620 630 640
LSPRLQYFGQSLGGQDLTMDGLVLTGAGQHVLLRSQPLVRVKAIMEFNFREVARNVFECNDQVVKGE
LSPRLQYFGQSLGGQDLTMDGLVLTGAGQHVLLRSQPLVRVKAIMEFNFREVARNVFECNDQVVKGE
LSPRLQYFGQSLGGQDLTMDGLVLTGAGQHVLLRSQPLVRVKAIMEFNFREVARNVFECNDQVVKGE
570 580 590 600 610 620 630
650 660 670 680 690 700 710 720
AGEVRVCLHVQKSTRDLREGQIQSVVTVYDLALDSGRPHSRAVENETKSTRQTVGLTQTCETLKLQLP
AGEVRVCLHVQKSTRDLREGQIQSVVTVYDLALDSGRPHSRAVENETKSTRQTVGLTQTCETLKLQLP
AGEVRVCLHVQKSTRDLREGQIQSVVTVYDLALDSGRPHSRAVENETKSTRQTVGLTQTCETLKLQLP
640 650 660 670 680 690 700
730 740 750 760 770 780 790
NCIEDPVSPIVLRNFSLVGTPLSAFGLNRPVLAEDAQRLFTALFPPEKCGNDNICODDLSITFSPMSLDC
NCIEDPVSPIVLRNFSLVGTPLSAFGLNRPVLAEDAQRLFTALFPPEKCGNDNICODDLSITFSPMSLDC
NCIEDPVSPIVLRNFSLVGTPLSAFGLNRPVLAEDAQRLFTALFPPEKCGNDNICODDLSITFSPMSLDC
710 720 730 740 750 760 770
LVVGGPREFNVTVTRNDGDSYRTQVTFPPFLDLSYKYSTLQNSQSRSLACSSASTEVSGALKSTS
LVVGGPREFNVTVTRNDGDSYRTQVTFPPFLDLSYKYSTLQNSQSRSLACSSASTEVSGALKSTS
LVVGGPREFNVTVTRNDGDSYRTQVTFPPFLDLSYKYSTLQNSQSRSLACSSASTEVSGALKSTS
780 790 800 810 820 830 840
CSINHPIFPENSEVTFNITFDVDSKASLGNKLLKANVTSENMMPTNKTEFQLELPVKYAVVMTSHGVS
CSINHPIFPENSEVTFNITFDVDSKASLGNKLLKANVTSENMMPTNKTEFQLELPVKYAVVMTSHGVS
CSINHPIFPENSEVTFNITFDVDSKASLGNKLLKANVTSENMMPTNKTEFQLELPVKYAVVMTSHGVS
870 880 890 900 910 920 930
TKYLNFTASENTSRMHOHQVSNLQSRSLPISLVPVFLNQTIVDRPQVTFSENLSSTCHTKERLPSH
TKYLNFTASENTSRMHOHQVSNLQSRSLPISLVPVFLNQTIVDRPQVTFSENLSSTCHTKERLPSH
TKYLNFTASENTSRMHOHQVSNLQSRSLPISLVPVFLNQTIVDRPQVTFSENLSSTCHTKERLPSH
940 950 960 970 980 990 1000
SDFLAERKAPVNCSTAVCORIQDIPPCGQIOEFNATKGNLSPDWYIKTSHNHLIVSTABILFNDVSF
SDFLAERKAPVNCSTAVCORIQDIPPCGQIOEFNATKGNLSPDWYIKTSHNHLIVSTABILFNDVSF
SDFLAERKAPVNCSTAVCORIQDIPPCGQIOEFNATKGNLSPDWYIKTSHNHLIVSTABILFNDVSF
1010 1020 1030 1040 1050 1060 1070 1080
TLPCQAGAFVSQETKVEPEVFNPLPLIVGSSVGGLLLLALITAAALYKLGFFKROYKDMWSEGGPPGARP
TLPCQAGAFVSQETKVEPEVFNPLPLIVGSSVGGLLLLALITAAALYKLGFFKROYKDMWSEGGPPGARP
TLPCQAGAFVSQETKVEPEVFNPLPLIVGSSVGGLLLLALITAAALYKLGFFKROYKDMWSEGGPPGARP
1090 1100 1110 1120 1130 1140 1150
TLPCQAGAFVSQETKVEPEVFNPLPLIVGSSVGGLLLLALITAAALYKLGFFKROYKDMWSEGGPPGARP
TLPCQAGAFVSQETKVEPEVFNPLPLIVGSSVGGLLLLALITAAALYKLGFFKROYKDMWSEGGPPGARP
TLPCQAGAFVSQETKVEPEVFNPLPLIVGSSVGGLLLLALITAAALYKLGFFKROYKDMWSEGGPPGARP
1160 1170 1180 1190 1200 1210 1220
X
Q
Q
Q
X

LENGTH: 1137
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
Initial Score = 1128 Optimized Score = 1128 Significance = 0.00
Residue Identity = 99% Matches = 1128 Mismatches = 9
Gaps = 0 Conservative Substitutions = 0
10 X 20 30 40 50 60 70
MALRVLLLTALTCHEGFLNDTENAMTFQENARGFGQSVVQLOGSRVVGAPOBIVAAANORGSLYQCYDSTGS
|||||
FNLDTENAMTFQENARGFGQSVVQLOGSRVVGAPOBIVAAANORGSLYQCYDSTGS
X 10 20 30 40 50
80 90 100 110 120 130 140
CEPIRLQVPVEAVNMSLGLSLAATSPPOLLAGCPVTHQTCSENTYVKGCLFLGSLNLRQPOKPFPEALRGC
|||||
CEPIRLQVPVEAVNMSLGLSLAATSPPOLLAGCPVTHQTCSENTYVKGCLFLGSLNLRQPOKPFPEALRGC
60 70 80 90 100 110 120
CEPIRLQVPVEAVNMSLGLSLAATSPPOLLAGCPVTHQTCSENTYVKGCLFLGSLNLRQPOKPFPEALRGC
|||||
POSDSDIAFLIDGSGSIIIPHDPRMKEFVSTYMEQLKSKTLPFLSMOYSEEPRIHFTFKFQNNPNSRLVK
|||||
POSDSDIAFLIDGSGSIIIPHDPRMKEFVSTYMEQLKSKTLPFLSMOYSEEPRIHFTFKFQNNPNSRLVK
130 140 150 160 170 180 190 200
PITQLLGRTHATATGIRKVVRELFNITNGARKNAFKILWITDGEKFGDPLGYEDVPEADREGVIRYVIGV
|||||
PITQLLGRTHATATGIRKVVRELFNITNGARKNAFKILWITDGEKFGDPLGYEDVPEADREGVIRYVIGV
210 220 230 240 250 260 270
PITQLLGRTHATATGIRKVVRELFNITNGARKNAFKILWITDGEKFGDPLGYEDVPEADREGVIRYVIGV
|||||
DAFRSEKSRQELNTIASKPRDHPVQNNFEALKTTONQRLREKIFAEGTQTGSSSFHEMSQEGESAALT
|||||
DAFRSEKSRQELNTIASKPRDHPVQNNFEALKTTONQRLREKIFAEGTQTGSSSFHEMSQEGESAALT
280 290 300 310 320 330 340
DAFRSEKSRQELNTIASKPRDHPVQNNFEALKTTONQRLREKIFAEGTQTGSSSFHEMSQEGESAALT
|||||
SNPGLLSTVGSYDWAGGVFLYTSKEKSTFINMTTRVDSMDNDAYLGVAAILNRVQSLVGLAPRYOHIGLV
|||||
SNPGLLSTVGSYDWAGGVFLYTSKEKSTFINMTTRVDSMDNDAYLGVAAILNRVQSLVGLAPRYOHIGLV
350 360 370 380 390 400 410 420 430
SNPGLLSTVGSYDWAGGVFLYTSKEKSTFINMTTRVDSMDNDAYLGVAAILNRVQSLVGLAPRYOHIGLV
|||||
AMFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLVIGAPHYVETRGQGVSVCPPLRGORARW
|||||
AMFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLVIGAPHYVETRGQGVSVCPPLRGORARW
420 430 440 450 460 470 480
AMFRONTGMWESNANVKGTOIGAYFGASLCSVDVDSNGSTDVLVIGAPHYVETRGQGVSVCPPLRGORARW
|||||
QCDVAVYXGEOGQPKWREFGMAALTVDLVGVDNGDKLTDVAIGAPQEDNRCAGVYLPHGTSGSGISPSHSQRIAGSK
|||||
QCDVAVYXGEOGQPKWREFGMAALTVDLVGVDNGDKLTDVAIGAPQEDNRCAGVYLPHGTSGSGISPSHSQRIAGSK
490 500 510 520 530 540 550 560 570
QCDVAVYXGEOGQPKWREFGMAALTVDLVGVDNGDKLTDVAIGAPQEDNRCAGVYLPHGTSGSGISPSHSQRIAGSK
|||||
580 590 600 610 620 630 640
LSPRLQYFGQSLGGQDLTMDGLVLTGAGQHVLLRSQPLVRVKAIMEFNFREVARNVFECNDQVVKGE
|||||
LSPRLQYFGQSLGGQDLTMDGLVLTGAGQHVLLRSQPLVRVKAIMEFNFREVARNVFECNDQVVKGE
LSPRLQYFGQSLGGQDLTMDGLVLTGAGQHVLLRSQPLVRVKAIMEFNFREVARNVFECNDQVVKGE
570 580 590 600 610 620 630
650 660 670 680 690 700 710 720
AGEVRVCLHVQKSTRDLREGQIQSVVTVYDLALDSGRPHSRAVENETKSTRQTVGLTQTCETLKLQLP
AGEVRVCLHVQKSTRDLREGQIQSVVTVYDLALDSGRPHSRAVENETKSTRQTVGLTQTCETLKLQLP
AGEVRVCLHVQKSTRDLREGQIQSVVTVYDLALDSGRPHSRAVENETKSTRQTVGLTQTCETLKLQLP
640 650 660 670 680 690 700
730 740 750 760 770 780 790
NCIEDPVSPIVLRNFSLVGTPLSAFGLNRPVLAEDAQRLFTALFPPEKCGNDNICODDLSITFSPMSLDC
NCIEDPVSPIVLRNFSLVGTPLSAFGLNRPVLAEDAQRLFTALFPPEKCGNDNICODDLSITFSPMSLDC
NCIEDPVSPIVLRNFSLVGTPLSAFGLNRPVLAEDAQRLFTALFPPEKCGNDNICODDLSITFSPMSLDC

3. US-09-902-481B-1 (1-1153)
US-09-902-481B-4 Sequence 4, Application US/09902481B

Sequence 4, Application US/09902481B
GENERAL INFORMATION:
APPLICANT: Springer, Timothy
APPLICANT: Shimooka, Motomu
APPLICANT: Shifman, Julia
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RPT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/502,481B
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/216,600
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4

NCIEDPVPSPVLRNLSVLTGTPSAGNRLVLAEDAQRFTALPPEKCKGNDNICQDDLSITSPMSLDC
710 720 730 740 750 760 770
800 810 820 830 840 850 860
LVVGGPREFNVTVVRNDGDSYRTQVTFPPFLDLSYKVKSTLQNSQSRWRLACESASSTEVSGALKSTS
LVVGGPREFNVTVVRNDGDSYRTQVTFPPFLDLSYKVKSTLQNSQSRWRLACESASSTEVSGALKSTS
780 790 800 810 820 830 840
870 880 890 900 910 920 930
CSINHPIPPENSEVTFNITFDVDSKASIGNKLLKANVTSENMPRTNKTFFQLELPVKYAVYVTVSHGVS
CSINHPIPPENSEVTFNITFDVDSKASIGNKLLKANVTSENMPRTNKTFFQLELPVKYAVYVTVSHGVS
850 860 870 880 890 900 910 920
940 950 960 970 980 990 1000
TKYLNFTASENTRSMQHQYQVSNLQSRSLPISLVFLVPRLNQTVIWRDQVTFSENLSSTCHTKERLPESH
TKYLNFTASENTRSMQHQYQVSNLQSRSLPISLVFLVPRLNQTVIWRDQVTFSENLSSTCHTKERLPESH
930 940 950 960 970 980 990
1010 1020 1030 1040 1050 1060 1070 1080
SDFLAELKAPVNCIAVCORIQDIPFGIOEHPNATLKNLSFDWYIKTSNHLILVSTABILFNDSVF
SDFLAELKAPVNCIAVCORIQDIPFGIOEHPNATLKNLSFDWYIKTSNHLILVSTABILFNDSVF
1000 1010 1020 1030 1040 1050 1060
1090 1100 1110 1120 1130 1140 1150
TLFQCGAFVSQSTETKVEPEVNPPLIVGSSVGGLLALITAAKYLGFFKQYKDMMSGGPPGABP
TLFQCGAFVSQSTETKVEPEVNPPLIVGSSVGGLLALITAAKYLGFFKQYKDMMSGGPPGABP
1070 1080 1090 1100 1110 1120 1130
X
Q
Q
Q
X

4. US-09-902-481B-1 (1-1153)
US-09-902-481B-3 Sequence 3, Application US/09902481B
Sequence 3, Application US/09902481B
GENERAL INFORMATION:
APPLICANT: Springer, Timothy
APPLICANT: Shimooka, Motomu
APPLICANT: Shifman, Julia
APPLICANT: Mayo, Stephen
TITLE OF INVENTION: NOVEL PROTEINS WITH INTEGRIN-LIKE ACTIVITY
FILE REFERENCE: A-70586-1/RPT/RMS/RMK
CURRENT APPLICATION NUMBER: US/09/902,481B
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/216,600
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 1137
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic
Initial Score = 1124 Optimized Score = 1124 Significance = -1.08
Residue Identity = 98% Matches = 1124 Mismatches = 13
Gaps = 0 Conservative Substitutions = 0
10 X 20 30 40 50 60 70
MALRVLLLTALTICGHNLTENAMTFQENARGQSVVQLOGSRVWVGAPQEIIVAAQVQSGLYOCDSYTG
FNLDTENAMTFQENARGQSVVQLOGSRVWVGAPQEIIVAAQVQSGLYOCDSYTG
X 10 20 30 40 50

80 90 100 110 120 130 140
CEPIRLQVPVEAVNMSLGLSLAFTSPPOLLAGCPVHQCSTNTVKGCLFGLGNLRQOPKPFALRGC
CEPIRLQVPVEAVNMSLGLSLAFTSPPOLLAGCPVHQCSTNTVKGCLFGLGNLRQOPKPFALRGC
60 70 80 90 100 110 120
150 160 170 180 190 200 210
PQSDSIAFLIDSGSIIIPHDPRMKEFVSTVMBQKSKTFLSLQVSEEFRIHFTFKFQNNPRLSVK
PQSDSIAFLIDSGSIIIPHDPRMKEFVSTVMBQKSKTFLSLQVSEEFRIHFTFKFQNNPRLSVK
130 140 150 160 170 180 190 200
PITQLLGRTHATGLRVKVEELFNIENGARKNAFKILFILLTDGKEGDPGLGYEDVPELDRGVIRYVLF
PITQLLGRTHATGLRVKVEELFNIENGARKNAFKILFILLTDGKEGDPGLGYEDVPELDRGVIRYVLF
210 220 230 240 250 260 270 280
290 300 310 320 330 340 350 360
DAFRSEKSRQELNTIASKPPDRHVFQNNPFEALKTIONQLREKIFAIEGTQTSSTSSPHEMSQEGESAIT
DAFRSEKSRQELNTIASKPPDRHVFQNNPFEALKTIONQLREKIFAIEGTQTSSTSSPHEMSQEGESAIT
280 290 300 310 320 330 340
370 380 390 400 410 420 430
SNGPLLSTVGSYDWAGGVFLYTSKESKSTFINMTVRVSDMDAYLGYAAAIHNRVQSLVGLGAPRYOHILV
SNGPLLSTVGSYDWAGGVFLYTSKESKSTFINMTVRVSDMDAYLGYAAAIHNRVQSLVGLGAPRYOHILV
350 360 370 380 390 400 410
440 450 460 470 480 490 500
AMFRONTGMESNANVKGTOIGAYFGASLCSVDVDSNGSTDLVLIGAPHYETGTRGQSVVCLPQCORARW
AMFRONTGMESNANVKGTOIGAYFGASLCSVDVDSNGSTDLVLIGAPHYETGTRGQSVVCLPQCORARW
420 430 440 450 460 470 480
510 520 530 540 550 560 570
QCDAYLXGEOGQWGRFGAALTWGLGVNGDKLTDVAIGAPGEDNRCVAVLFGTSGSISPSHSQRIAGSK
QCDAYLXGEOGQWGRFGAALTWGLGVNGDKLTDVAIGAPGEDNRCVAVLFGTSGSISPSHSQRIAGSK
490 500 510 520 530 540 550 560
580 590 600 610 620 630 640
LSPRLQYFGQSLSGQDLTMDGLVLDLVGAQGHVLLRSQVLRVKAIMEFNFREAVARNVFECDQVVRGKE
LSPRLQYFGQSLSGQDLTMDGLVLDLVGAQGHVLLRSQVLRVKAIMEFNFREAVARNVFECDQVVRGKE
570 580 590 600 610 620 630
650 660 670 680 690 700 710 720
AGEVRVCLHVKQSTRDLRREGQIQSVVYTDLALDSGRPHSRVAFNETKNSTRQTVLGLTQTCETLKLQLP
AGEVRVCLHVKQSTRDLRREGQIQSVVYTDLALDSGRPHSRVAFNETKNSTRQTVLGLTQTCETLKLQLP
640 650 660 670 680 690 700
730 740 750 760 770 780 790
NCIEDPVPSPVLRNLSVLTGTPSAGNRLVLAEDAQRFTALPPEKCKGNDNICQDDLSITSPMSLDC
NCIEDPVPSPVLRNLSVLTGTPSAGNRLVLAEDAQRFTALPPEKCKGNDNICQDDLSITSPMSLDC
710 720 730 740 750 760 770
800 810 820 830 840 850 860
LVVGGPREFNVTVVRNDGDSYRTQVTFPPFLDLSYKVKSTLQNSQSRWRLACESASSTEVSGALKSTS
LVVGGPREFNVTVVRNDGDSYRTQVTFPPFLDLSYKVKSTLQNSQSRWRLACESASSTEVSGALKSTS
780 790 800 810 820 830 840
870 880 890 900 910 920 930
CSINHPIPPENSEVTFNITFDVDSKASIGNKLLKANVTSENMPRTNKTFFQLELPVKYAVYVTVSHGVS
CSINHPIPPENSEVTFNITFDVDSKASIGNKLLKANVTSENMPRTNKTFFQLELPVKYAVYVTVSHGVS
850 860 870 880 890 900 910 920

940 950 960 970 980 990 1000
TKYLNFTASNTSRVMOHQYQVSNLQORSIPISLVLPVRLNQTVMRPOVTFSENLSSTCHTKERLP
TKYLNFTASNTSRVMOHQYQVSNLQORSIPISLVLPVRLNQTVMRPOVTFSENLSSTCHTKERLP
TKYLNFTASNTSRVMOHQYQVSNLQORSIPISLVLPVRLNQTVMRPOVTFSENLSSTCHTKERLP
930 940 950 960 970 980 990
1010 1020 1030 1040 1050 1060 1070 1080
SDFLAELRKAPVNCIAVCQRIQCDIPFFGIQEEFNATLKGNSLFDWYIKTSHNHLIVSTAEILFND
SDFLAELRKAPVNCIAVCQRIQCDIPFFGIQEEFNATLKGNSLFDWYIKTSHNHLIVSTAEILFND
SDFLAELRKAPVNCIAVCQRIQCDIPFFGIQEEFNATLKGNSLFDWYIKTSHNHLIVSTAEILFND
1000 1010 1020 1030 1040 1050 1060
1090 1100 1110 1120 1130 1140 1150
TLIPGGGAFVRSQTETKVEPFVFNPLPIVSGSGLLALITAAALYKLGFFKQYKDMMSGGPPGAEP
TLIPGGGAFVRSQTETKVEPFVFNPLPIVSGSGLLALITAAALYKLGFFKQYKDMMSGGPPGAEP
TLIPGGGAFVRSQTETKVEPFVFNPLPIVSGSGLLALITAAALYKLGFFKQYKDMMSGGPPGAEP
1070 1080 1090 1100 1110 1120 1130

x
Q
Q
Q
x


```
|||||
US-09-902- 412 HIGLVAFQNTGMWESNANVAGTQIGAYFGASLCSVDVDSNGSDLDVLIGAPHYYEQTRG
|||||
US-09-902- 412 HIGLVAFQNTGMWESNANVAGTQIGAYFGASLCSVDVDSNGSDLDVLIGAPHYYEQTRG
|||||
US-09-902- 428 HIGLVAFQNTGMWESNANVAGTQIGAYFGASLCSVDVDSNGSDLDVLIGAPHYYEQTRG
|||||
consensus
higlvamfrqntgmwesanvkgtdqigayfgaslcsvdvdsngstdldvligaphyyeqtrg

US-09-902- 1
|||||
US-09-902- 473 GQVSVCPLPRGQARWQCDVALYGEQGPWGRFGAALTVLGDVNGDKLTDVAIGAPGEDN
|||||
US-09-902- 473 GQVSVCPLPRGQARWQCDVALYGEQGPWGRFGAALTVLGDVNGDKLTDVAIGAPGEDN
|||||
US-09-902- 473 GQVSVCPLPRGQARWQCDVALYGEQGPWGRFGAALTVLGDVNGDKLTDVAIGAPGEDN
|||||
US-09-902- 473 GQVSVCPLPRGQARWQCDVALYGEQGPWGRFGAALTVLGDVNGDKLTDVAIGAPGEDN
|||||
US-09-902- 489 GQVSVCPLPRGQARWQCDVALYGEQGPWGRFGAALTVLGDVNGDKLTDVAIGAPGEDN
|||||
consensus
gqvsvcplprgqrarwqcdvalygeqgpwgrfgaaltvlgdvngdkltdvaigapgedn

US-09-902- 1
|||||
US-09-902- 534 RGAVYLFHGTSGSGISPSHSORITAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHV
|||||
US-09-902- 534 RGAVYLFHGTSGSGISPSHSORITAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHV
|||||
US-09-902- 534 RGAVYLFHGTSGSGISPSHSORITAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHV
|||||
US-09-902- 534 RGAVYLFHGTSGSGISPSHSORITAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHV
|||||
US-09-902- 550 RGAVYLFHGTSGSGISPSHSORITAGSKLSPRLQYFGQSLSGGQDLTMDGLVDLTVGAQGHV
|||||
consensus
rgavylfhgtsgsgispshsoriagsklsprlqyfgqslsggqdltdmdglvdltvgaqghv

US-09-902- 1
|||||
US-09-902- 595 LLRSQPVLRVKAIMFNPREVARNVFECDQVVKGEAGEVRVCLHVQKSTRDLRREGQI
|||||
US-09-902- 595 LLRSQPVLRVKAIMFNPREVARNVFECDQVVKGEAGEVRVCLHVQKSTRDLRREGQI
|||||
US-09-902- 595 LLRSQPVLRVKAIMFNPREVARNVFECDQVVKGEAGEVRVCLHVQKSTRDLRREGQI
|||||
US-09-902- 595 LLRSQPVLRVKAIMFNPREVARNVFECDQVVKGEAGEVRVCLHVQKSTRDLRREGQI
|||||
US-09-902- 611 LLRSQPVLRVKAIMFNPREVARNVFECDQVVKGEAGEVRVCLHVQKSTRDLRREGQI
|||||
consensus
lllrsqpvrlrvkaimfnprevarnvfeecdqvvgkgeagevrvcclhvqkstrdlrregqi

US-09-902- 1
|||||
US-09-902- 656 QSVVYDLDLDSGRPHSAFVNETKSTRQTQVLGTLQTCETLKLQLPNCIEDPVSPIVL
|||||
US-09-902- 656 QSVVYDLDLDSGRPHSAFVNETKSTRQTQVLGTLQTCETLKLQLPNCIEDPVSPIVL
|||||
US-09-902- 656 QSVVYDLDLDSGRPHSAFVNETKSTRQTQVLGTLQTCETLKLQLPNCIEDPVSPIVL
|||||
US-09-902- 656 QSVVYDLDLDSGRPHSAFVNETKSTRQTQVLGTLQTCETLKLQLPNCIEDPVSPIVL
|||||
US-09-902- 672 QSVVYDLDLDSGRPHSAFVNETKSTRQTQVLGTLQTCETLKLQLPNCIEDPVSPIVL
|||||
consensus
qsvvtydldldsgprhsafvnetkstrqtqvlgtlqtccetlklqlpnciedpvspivl

US-09-902- 1
|||||
US-09-902- 717 RLNFSLVGTPLSAFGLNRPVLAEDAQRLFTALFPFKNCGNDNICODDLSITFSFMSLDCL
```

```
|||||
US-09-902- 717 RLNFSLVGTPLSAFGLNRPVLAEDAQRLFTALFPFKNCGNDNICODDLSITFSFMSLDCL
|||||
US-09-902- 717 RLNFSLVGTPLSAFGLNRPVLAEDAQRLFTALFPFKNCGNDNICODDLSITFSFMSLDCL
|||||
US-09-902- 717 RLNFSLVGTPLSAFGLNRPVLAEDAQRLFTALFPFKNCGNDNICODDLSITFSFMSLDCL
|||||
US-09-902- 733 RLNFSLVGTPLSAFGLNRPVLAEDAQRLFTALFPFKNCGNDNICODDLSITFSFMSLDCL
|||||
consensus
rlnfslvgtplsaafgnlrpvlaedaqrifltalfpfknecndnicqddlsitfmsldcl

US-09-902- 1
|||||
US-09-902- 778 VVGGRPREFNVTVTVRNDGEDSYRTQVTFFPPLDLSYRKVSTLQORSQSRWLACESASST
|||||
US-09-902- 778 VVGGRPREFNVTVTVRNDGEDSYRTQVTFFPPLDLSYRKVSTLQORSQSRWLACESASST
|||||
US-09-902- 778 VVGGRPREFNVTVTVRNDGEDSYRTQVTFFPPLDLSYRKVSTLQORSQSRWLACESASST
|||||
US-09-902- 778 VVGGRPREFNVTVTVRNDGEDSYRTQVTFFPPLDLSYRKVSTLQORSQSRWLACESASST
|||||
US-09-902- 778 VVGGRPREFNVTVTVRNDGEDSYRTQVTFFPPLDLSYRKVSTLQORSQSRWLACESASST
|||||
US-09-902- 794 VVGGRPREFNVTVTVRNDGEDSYRTQVTFFPPLDLSYRKVSTLQORSQSRWLACESASST
|||||
consensus
vvggprefnvtvtrndgedsyrtqvtffppldlsyrkvstlqnrswrlacesasst

US-09-902- 1
|||||
US-09-902- 839 EVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKANTSENMPRTNKTE
|||||
US-09-902- 839 EVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKANTSENMPRTNKTE
|||||
US-09-902- 839 EVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKANTSENMPRTNKTE
|||||
US-09-902- 839 EVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKANTSENMPRTNKTE
|||||
US-09-902- 839 EVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKANTSENMPRTNKTE
|||||
US-09-902- 855 EVSGALKSTSCSINHPIPPENSEVTFNITFDVDSKASLGNKLLKANTSENMPRTNKTE
|||||
consensus
evsgalkstscsinhpifpensevtfnitfdvdsksaslgknllkanvtseumprtntkte

US-09-902- 1
|||||
US-09-902- 900 FOLELPVKYAVVMVVTSHGVSTKYLNFNTASENTSRVMQHQVSNLQORSLDISLVFLVPV
|||||
US-09-902- 900 FOLELPVKYAVVMVVTSHGVSTKYLNFNTASENTSRVMQHQVSNLQORSLDISLVFLVPV
|||||
US-09-902- 900 FOLELPVKYAVVMVVTSHGVSTKYLNFNTASENTSRVMQHQVSNLQORSLDISLVFLVPV
|||||
US-09-902- 900 FOLELPVKYAVVMVVTSHGVSTKYLNFNTASENTSRVMQHQVSNLQORSLDISLVFLVPV
|||||
US-09-902- 900 FOLELPVKYAVVMVVTSHGVSTKYLNFNTASENTSRVMQHQVSNLQORSLDISLVFLVPV
|||||
US-09-902- 916 FOLELPVKYAVVMVVTSHGVSTKYLNFNTASENTSRVMQHQVSNLQORSLDISLVFLVPV
|||||
consensus
fglelpvkvayvmvvtshgvstkylnftasentsrvmqhqvsnlgqrsipisvlvpv

US-09-902- 1
|||||
US-09-902- 961 RLNQTVINDRPOVTFSENLSSCTCHTKERLPSSHDFLAEIRKAPVNVNCISIAVCORIQCDIIPF
|||||
US-09-902- 961 RLNQTVINDRPOVTFSENLSSCTCHTKERLPSSHDFLAEIRKAPVNVNCISIAVCORIQCDIIPF
|||||
US-09-902- 961 RLNQTVINDRPOVTFSENLSSCTCHTKERLPSSHDFLAEIRKAPVNVNCISIAVCORIQCDIIPF
|||||
US-09-902- 961 RLNQTVINDRPOVTFSENLSSCTCHTKERLPSSHDFLAEIRKAPVNVNCISIAVCORIQCDIIPF
|||||
US-09-902- 977 RLNQTVINDRPOVTFSENLSSCTCHTKERLPSSHDFLAEIRKAPVNVNCISIAVCORIQCDIIPF
|||||
consensus
rlnqtvindrpoqvtfsenlssctchtkerlpshdsflaelrkapvvnvncisavcgricqcdipf

US-09-902- 1
|||||
```

```
US-09-902- 1022 FGIQEEFNATLKGNSLSPDWIKTSHNHLIIIVSTAELFNDVSFTLLPGQGFVRSQETETKV
|||||
US-09-902- 1022 FGIQEEFNATLKGNSLSPDWIKTSHNHLIIIVSTAELFNDVSFTLLPGQGFVRSQETETKV
|||||
US-09-902- 1022 FGIQEEFNATLKGNSLSPDWIKTSHNHLIIIVSTAELFNDVSFTLLPGQGFVRSQETETKV
|||||
US-09-902- 1022 FGIQEEFNATLKGNSLSPDWIKTSHNHLIIIVSTAELFNDVSFTLLPGQGFVRSQETETKV
|||||
US-09-902- 1022 FGIQEEFNATLKGNSLSPDWIKTSHNHLIIIVSTAELFNDVSFTLLPGQGFVRSQETETKV
|||||
US-09-902- 1038 FGIQEEFNATLKGNSLSPDWIKTSHNHLIIIVSTAELFNDVSFTLLPGQGFVRSQETETKV
|||||
consensus fgiqeefnatlkgnslsfdwiktshnhllivstaelfndsvftllpgggafvrsqetkv

US-09-902- 1 mgxxxxGGPP
|||||
US-09-902- 1083 EPFEVNPPLPIVGSVSGGLLALITAAALYKLGFFKQRYKDMMSGGPPGAEPPQ
|||||
US-09-902- 1083 EPFEVNPPLPIVGSVSGGLLALITAAALYKLGFFKQRYKDMMSGGPPGAEPPQ
|||||
US-09-902- 1083 EPFEVNPPLPIVGSVSGGLLALITAAALYKLGFFKQRYKDMMSGGPPGAEPPQ
|||||
US-09-902- 1083 EPFEVNPPLPIVGSVSGGLLALITAAALYKLGFFKQRYKDMMSGGPPGAEPPQ
|||||
US-09-902- 1099 EPFEVNPPLPIVGSVSGGLLALITAAALYKLGFFKQRYKDMMSGGPPGAEPPQ
|||||
consensus epfevnpplpivgssvgglllaltaaalykgffkrykdmmsGGPPgaeppq
```

Alignment score = -1505.00

Scoring matrix:

	1	2	3	4	5	6
1		1044	1048	1049	1053	-5711
2			1131	1124	1122	-5631
3				1129	1126	-5631
4					1127	-5631
5						-5631
6						
